OIPE

This Raw Listing contains the General
Information Section and up to the first 5 pages

ENTERED

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information
 4
 5           (i) APPLICANT: Au-Young, Janice
 6                          Lal, Preeti
 7                          Bandman, Olga
 8
 9           (ii) TITLE OF THE INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
10
11           (iii) NUMBER OF SEQUENCES: 7
12
13           (iv) CORRESPONDENCE ADDRESS:
14              (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15              (B) STREET: 3174 Porter Drive
16              (C) CITY: Palo Alto
17              (D) STATE: CA
18              (E) COUNTRY: USA
19              (F) ZIP: 94304
20
21           (v) COMPUTER READABLE FORM:
22              (A) MEDIUM TYPE: Diskette
23              (B) COMPUTER: IBM Compatible
24              (C) OPERATING SYSTEM: DOS
25              (D) SOFTWARE: FastSEQ for Windows Version 2.0
26
27           (vi) CURRENT APPLICATION DATA:
28              (A) APPLICATION NUMBER: To Be Assigned
29              (B) FILING DATE: Herewith
30
31           (vii) PRIOR APPLICATION DATA:
32              (A) APPLICATION NUMBER: 08/868,288
33              (B) FILING DATE: June 3, 1997
34
35              (A) APPLICATION NUMBER: 09/235,373
36              (B) FILING DATE: January 20, 1999
37
38              (A) APPLICATION NUMBER: 09/388,993
39              (B) FILING DATE: September 2, 1999
40
41           (viii) ATTORNEY/AGENT INFORMATION:
42              (A) NAME: Streeter, David G.
43              (B) REGISTRATION NUMBER: 43,168
44              (C) REFERENCE/DOCKET NUMBER: PF-0309-3 DIV
45
46           (ix) TELECOMMUNICATION INFORMATION:
```

INPUT SET: S34917.raw

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47              (A) TELEPHONE: 415-855-0555
48              (B) TELEFAX: 415-849-8886
49
50
51          (2) INFORMATION FOR SEQ ID NO:1:
52
53          (i) SEQUENCE CHARACTERISTICS:
54              (A) LENGTH: 358 amino acids
55              (B) TYPE: amino acid
56              (C) STRANDEDNESS: single
57              (D) TOPOLOGY: linear
58
59          (vii) IMMEDIATE SOURCE:
60              (A) LIBRARY: SYNORAB01
61              (B) CLONE: 136466
62
63          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65  Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu
66   1           5                  10                  15
67  Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val
68              20                  25                  30
69  Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu
70          35                  40                  45
71  Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln
72          50                  55                  60
73  Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser
74  65                  70                  75                  80
75  Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp
76              85                  90                  95
77  Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp
78              100                 105                 110
79  Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile
80          115                 120                 125
81  Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
82          130                 135                 140
83  Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
84  145                 150                 155                 160
85  Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
86              165                 170                 175
87  Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
88              180                 185                 190
89  Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
90              195                 200                 205
91  Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
92          210                 215                 220
93  Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
94  225                 230                 235                 240
95
96  Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
97              245                 250                 255
98  Asp Leu Tyr Thr Asn Val Thr Val Ser Leu Val Glu Ser Leu Val Gly
99              260                 265                 270
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INPUT SET: S34917.raw

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101            275                 280                 285
102    Arg Asp Lys Ile Thr Arg Pro Gly Ala Xaa Xaa Trp Lys Lys Gly Glu
103            290                 295                 300
104    Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
105    305                 310                 315                 320
106    Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
107            325                 330                 335
108    Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
109            340                 345                 350
110    Asn Gly Leu Gln Gly Tyr
111            355
112
113            (2) INFORMATION FOR SEQ ID NO:2:
114
115            (i) SEQUENCE CHARACTERISTICS:
116                (A) LENGTH: 1376 base pairs
117                (B) TYPE: nucleic acid
118                (C) STRANDEDNESS: single
119                (D) TOPOLOGY: linear
120
121            (vii) IMMEDIATE SOURCE:
122                (A) LIBRARY: SYNORAB01
123                (B) CLONE: 136466
124
125            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
126
127    TCTCACCGGG ACTCGGGACT CCCGGGAAGT GGACCGGCAG AAGAGGGGGC TAGCTAGCTG    60
128    TCTCTGCGGA CCAGGGAGAC CCCCGCGCCC CCCCGGTGTG AGGCGGCCTC ACAGGGCCGG   120
129    GTGGGCTGGC GAGCCGACGC GGCGGCGGAG GAGGCTGTGA GGAGTGTGTG GAACAGGACC   180
130    CGGGACAGAG GAACCATGGC TCCGCAGAAC CTGAGCACCT TTTGCCTGTT GCTGCTATAC   240
131    CTCATCGGGG CGGTGATTGC CGGACGAGAT TTCTATAAGA TCTTGGGGGT GCCTCGAAGT   300
132    GCCTCTATAA AGGATATTAA AAAGGCCTAT AGGAAACTAG CCCTGCAGCT TCATCCCGAC   360
133    CGGAACCCTG ATGATCCACA AGCCCAGGAG AAATTCCAGG ATCTGGGTGC TGCTTATGAG   420
134    GTTCTGTCAG ATAGTGAGAA ACGGAAACAG TACGATACTT ATGGTGAAGA AGGATTAAAA   480
135    GATGGTCATC AGAGCTCCCA TGGAGACATT TTTTCACACT TCTTTGGGGA TTTTGGTTTC   540
136    ATGTTTGGAG GAACCCCTCG TCAGCAAGAC AGAAATATTC CAAGAGGAAG TGATATTATT   600
137    GTAGATCTAG AAGTCACTTT GGAAGAAGTA TATGCAGGAA ATTTTGTGGA AGTAGTTAGA   660
138    AACAAACCTG TGGCAAGGCA GGCTCCTGGC AAACGGAAGT GCAATTGTCG GCAAGAGATG   720
139    CGGACCACCC AGCTGGGCCC TGGGCGCTTC CAAATGACCC AGGAGGTGGT CTGCGACGAA   780
140    TGCCCTAATG TCAAACTAGT GAATGAAGAA CGAACGCTGG AAGTAGAAAT AGAGCCTGGG   840
141    GTGAGAGACG GCATGGAGTA CCCCTTTATT GGAGAAGGTG AGCCTCACGT GGATGGGGAG   900
142    CCTGGAGATT TACGGTTCCG AATCAAAGTT GTCAAGCACC AATATTTGA AAGGAGAGGA   960
143    GATGATTTGT ACACAAATGT GACAGTCTCA TTAGTTGAGT CACTGGTTGG CTTTGAGATG  1020
144    GATATTACTC ACTTGGATGG TCACAAGGTA CATATTTCCC GGGATAAGAT CACCAGGCCA  1080
145    GGAGCGAANT ANTGGAAGAA AGGGGAAGGG CTCCCCAACT TTGACAACAA CAATATCAAG  1140
146    GGCTCTTTGA TAATCACTTT TGATGTGGAT TTTCCAAAAG AACAGTTAAC AGAGGAAGCG  1200
147    AGAGAAGGTA TCAAACAGCT ACTGAAACAA GGGTCAGTGC AGAAGGTATA CAATGGACTG  1260
148    CAAGGATATT GAGAGTGAAT AAAAATTGGAC TTTGTTTAAA ATAAGTGAAT AAGCGATATT  1320
149    TATTATCTGC AAGGTTTTTT TGTGTGTGTT TTTGTTTTTA TTTTCAATAT GCAAGT      1376
150
151            (2) INFORMATION FOR SEQ ID NO:3:
152
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153              (i) SEQUENCE CHARACTERISTICS:
154                  (A) LENGTH: 330 amino acids
155                  (B) TYPE: amino acid
156                  (C) STRANDEDNESS: single
157                  (D) TOPOLOGY: linear
158
159              (vii) IMMEDIATE SOURCE:
160                  (A) LIBRARY: HNT2RAT01
161                  (B) CLONE: 260873
162
163              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
164
165      Met Val Asp Tyr Tyr Glu Val Leu Gly Val Gln Arg His Ala Ser Pro
166      1               5                   10                  15
167      Glu Asp Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys Trp His Pro
168                  20                  25                  30
169      Asp Lys Asn Pro Glu Asn Lys Glu Glu Ala Glu Arg Lys Phe Lys Gln
170                  35                  40                  45
171      Val Ala Glu Ala Tyr Glu Val Leu Ser Asp Ala Lys Lys Arg Asp Ile
172          50                  55                  60
173      Tyr Asp Lys Tyr Gly Lys Glu Gly Leu Asn Gly Gly Gly Gly Gly Gly
174      65                  70                  75                      80
175      Ser His Phe Asp Ser Pro Phe Glu Phe Gly Phe Thr Phe Arg Asn Pro
176                  85                  90                  95
177      Asp Asp Val Phe Arg Glu Phe Phe Gly Gly Arg Asp Pro Phe Ser Phe
178                  100                 105                 110
179      Asp Phe Phe Glu Asp Pro Phe Glu Asp Phe Phe Gly Asn Arg Arg Gly
180                  115                 120                 125
181      Pro Arg Gly Ser Arg Ser Arg Gly Thr Gly Ser Phe Phe Ser Ala Phe
182          130                 135                 140
183      Ser Gly Phe Pro Ser Phe Gly Ser Gly Phe Ser Ser Phe Asp Thr Gly
184      145                 150                 155                 160
185      Phe Thr Ser Phe Gly Ser Leu Gly His Gly Gly Leu Thr Ser Phe Ser
186                  165                 170                 175
187      Ser Thr Ser Phe Gly Gly Ser Gly Met Gly Asn Phe Lys Ser Ile Ser
188                  180                 185                 190
189      Thr Ser Thr Lys Met Val Asn Gly Arg Lys Ile Thr Thr Lys Arg Ile
190                  195                 200                 205
191      Val Glu Asn Gly Gln Glu Arg Val Glu Val Glu Glu Asp Gly Gln Leu
192          210                 215                 220
193      Lys Ser Leu Thr Ile Asn Gly Val Ala Asp Asp Asp Ala Leu Xaa Glu
194      225                 230                 235                 240
195      Glu Arg Met Arg Arg Gly Gln Asn Val Leu Pro Ala Gln Pro Ala Gly
196                  245                 250                 255
197      Leu Arg Pro Pro Lys Pro Pro Arg Pro Ala Ser Leu Leu Arg His Xaa
198                  260                 265                 270
199      Pro His Cys Leu Ser Lys Glu Glu Gly Glu Gln Asp Arg Pro Trp Ala
200                  275                 280                 285
201      Pro Xaa Xaa Trp Xaa Pro Leu Ala Ser Xaa Ala Gly Xaa Xaa Glu Gly
202          290                 295                 300
203      Xaa Lys Arg Met Xaa Ala Glu Ala Glu Arg Gly Val Glu Glu Glu Glu
204      305                 310                 315                 320
205      Val Asp Gln Arg Gln Ser Leu Asp Arg Thr
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206                     325                 330
207
208          (2) INFORMATION FOR SEQ ID NO:4:
209
210      (i) SEQUENCE CHARACTERISTICS:
211          (A) LENGTH: 1330 base pairs
212          (B) TYPE: nucleic acid
213          (C) STRANDEDNESS: single
214          (D) TOPOLOGY: linear
215
216      (vii) IMMEDIATE SOURCE:
217          (A) LIBRARY: HNT2RAT01
218          (B) CLONE: 260873
219
220
221      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
222
223
224  CGNAGGAGAG NAAAGGAAAG NCGCCGCAGG AGCCGCCGCN ACCACCAGCG NCACANTCCT      60
225  GGNGCTNTGA GGAGATTCGG GCCGTCACCC TGCCTCCCCT GCTTCCCGCC ACCGGCCGCT     120
226  TCTTTCCTCG GACCCATTCC AACAATCTCG TAAAACATGG TGGATTACTA TGAAGTTCTA     180
227  GGCGTGCAGA GACATGCCTC ACCCGAGGAT ATTAAAAAGG CATATCGGAA ACTGGCACTG     240
228  AAGTGGCATC CAGATAAAAA TCCTGAGAAT AAAGAAGAAG CAGAGAGAAA ATTCAAGCAA     300
229  GTAGCGGAGG CATATGAAGT GCTGTCGGAT GCTAAGAAAC GGGACATCTA TGACAAATAT     360
230  GGCAAAGAAG GATTAAATGG TGGNGGNGGN GGTGGAAGTC ATTTTGACAG TCCATTTGAA     420
231  TTTGGCTTCA CATTCCGTAA CCCAGATGAT GTCTTCAGGG AATTTTTTGG TGGAAGGGAC     480
232  CCATTTTCAT TTGACTTCTT TGAAGACCCT TTTGAGGACT TCTTTGGGAA TCGAAGGGGT     540
233  CCCCGAGGAA GCAGAAGCCG AGGGACGGGG TCGTTTTTCT CTGCGTTCAG TGGATTTCCG     600
234  TCTTTTGGAA GTGGATTTTC TTCTTTTGAT ACAGGATTTA CTTCATTTGG GTCACTAGGT     660
235  CACGGGGGCC TCACTTCATT CTCTTCCACG TCATTTGGTG GTAGTGGCAT GGGCAACTTC     720
236  AAATCGATAT CAACTTCAAC TAAAATGGTT AATGGCAGAA AAATCACTAC AAAGAGAATT     780
237  GTCGAGAACG GTCAAGAAAG AGTAGAAGTT GAAGAAGATG GCCAGTTAAA GTCCTAACA      840
238  ATAAATGGTG TKGCCGACGA CGATGCCCTC GSTGAGGAGC GCATGCGGAG AGGCCAGAAC     900
239  GTCCTGCCAG CCCAGCCTGC CGGCCTCCGA CCGCCGAAGC CGCCCCGGCC TGCCTCGTTG     960
240  CTGAGACACG NGCCTCATTG TCTCTCTAAG GAGGAGGGCG AGCAGGACCG ACCTTGGGCA    1020
241  CCCGNGNCCT GGNNCCCCCT CGCTTCCNCA GCAGGNTTNN AAGAAGGTNG CAAGAGGATG    1080
242  NAAGCAGAAG CAGAGAGAGG AGTCGAAGAA GAAGAAGTCG ACCAAAGGCA ATCACTAGAC    1140
243  CGGACTTGAG GCACGCGGTG CACCCCCAGA CGCTGGCGCT CCACCGTGCT CGGCATGCGG    1200
244  TCGTGCACAC GCGCTAGGTA GCAGCGTCGG TCAGGACTGT CTCGAGGCCA CACTCGCTCG    1260
245  GCAGGATTAT GCGATCACGG ATCAGTCAGA GCAGGGTCAG GAGACGGGGC TGACGGCACG    1320
246  GGTGGCGGGG                                                          1330
247
248          (2) INFORMATION FOR SEQ ID NO:5:
249
250      (i) SEQUENCE CHARACTERISTICS:
251          (A) LENGTH: 397 amino acids
252          (B) TYPE: amino acid
253          (C) STRANDEDNESS: single
254          (D) TOPOLOGY: linear
255
256      (vii) IMMEDIATE SOURCE:
257          (A) LIBRARY: GenBank
258          (B) CLONE: 306714
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/501,714*

INPUT SET: S34917.raw

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: To Be Assigned